

Figure 1A.

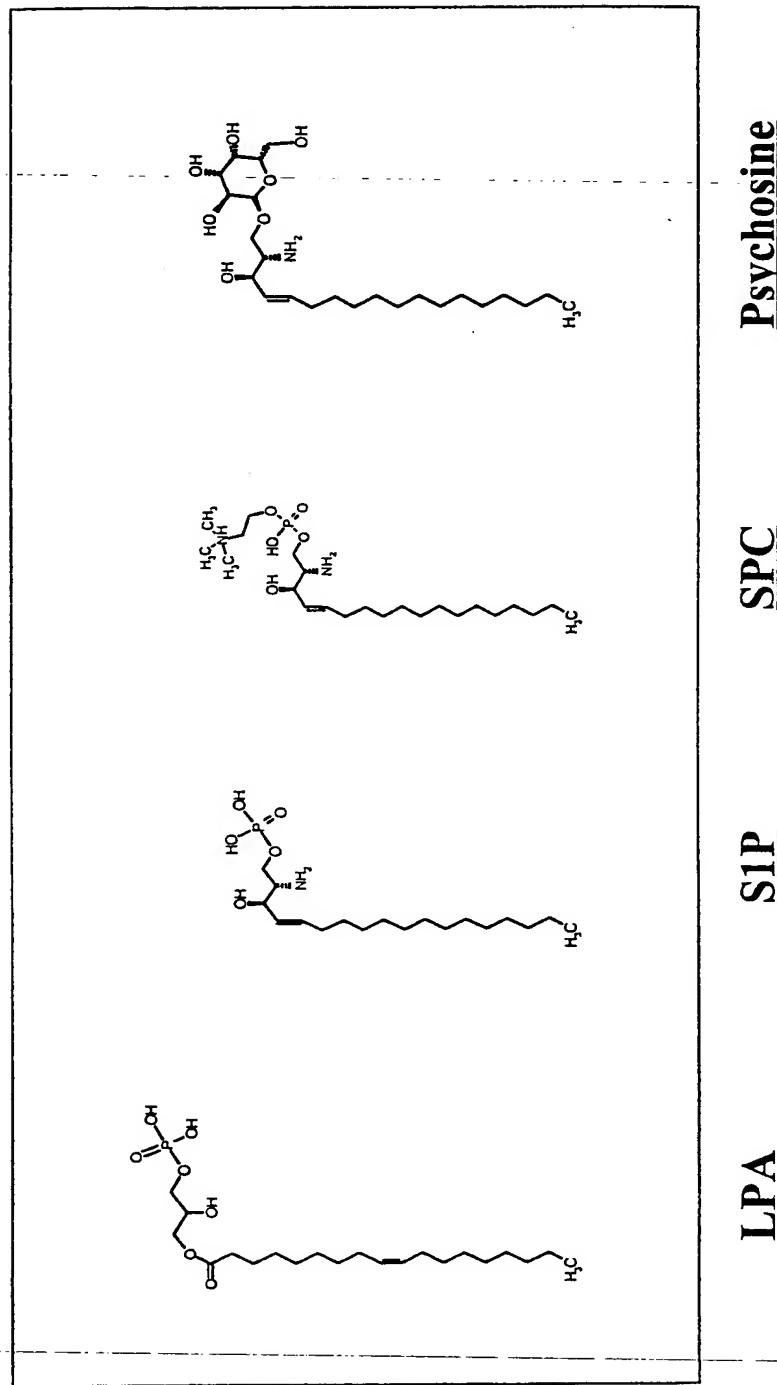


Figure 1B.

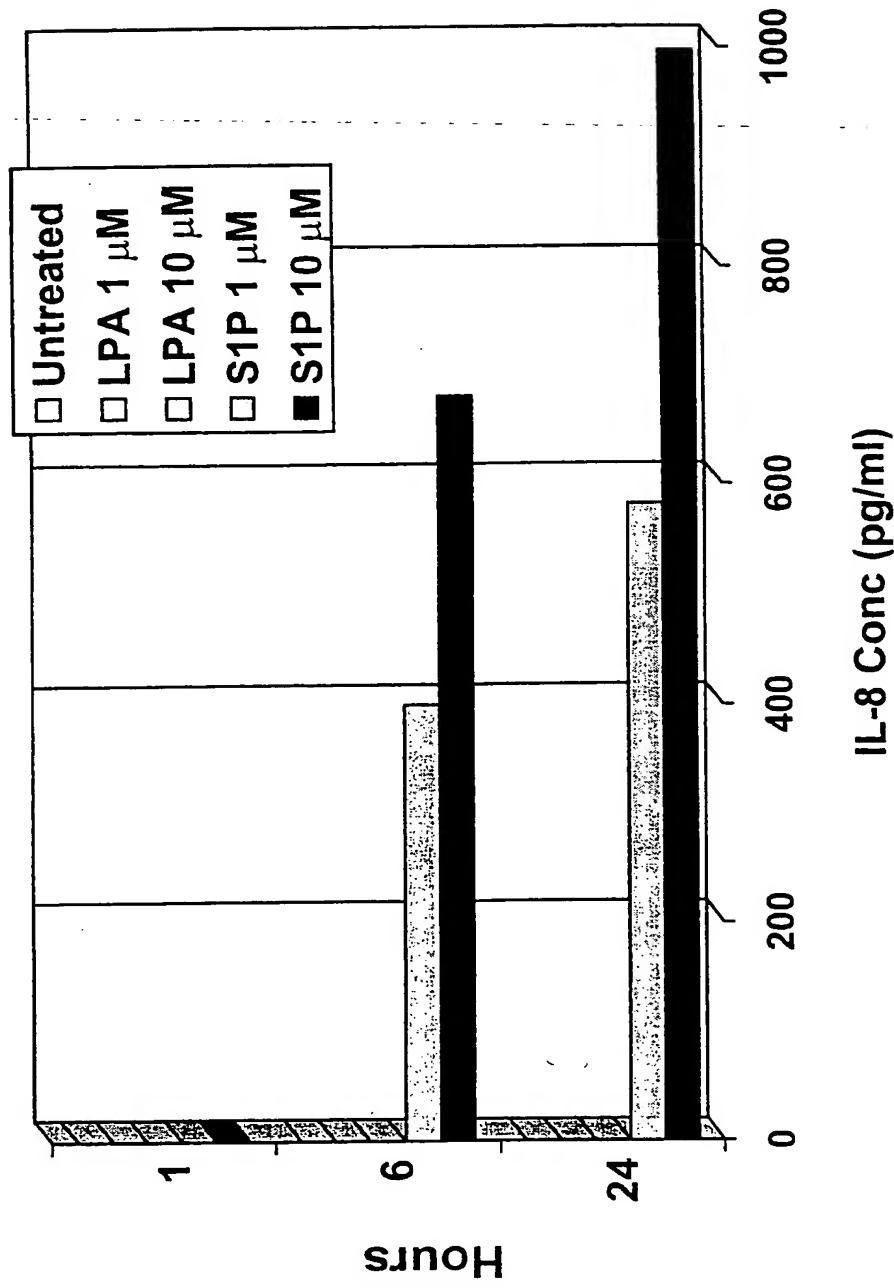


Figure 2A.

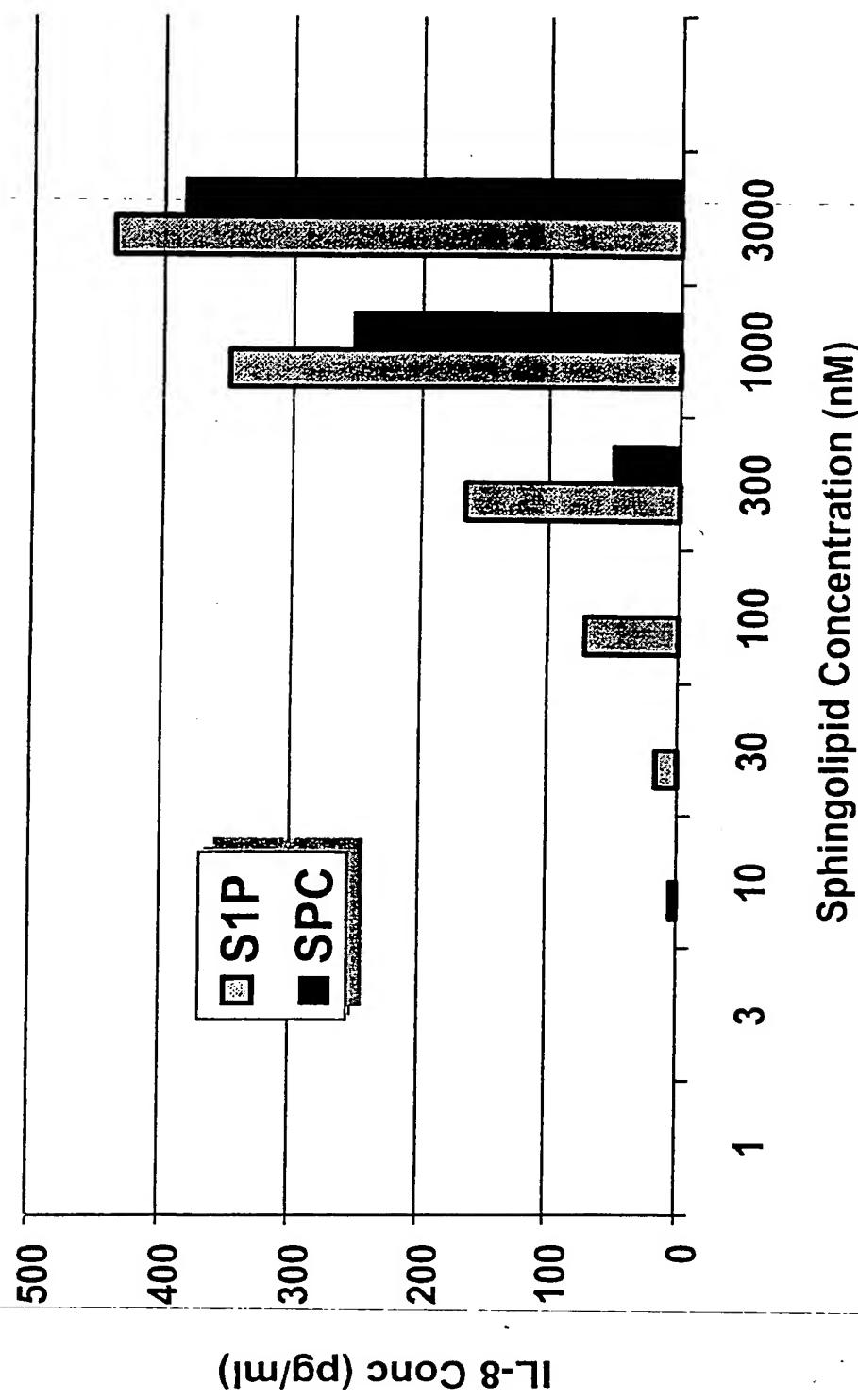


FIGURE 2

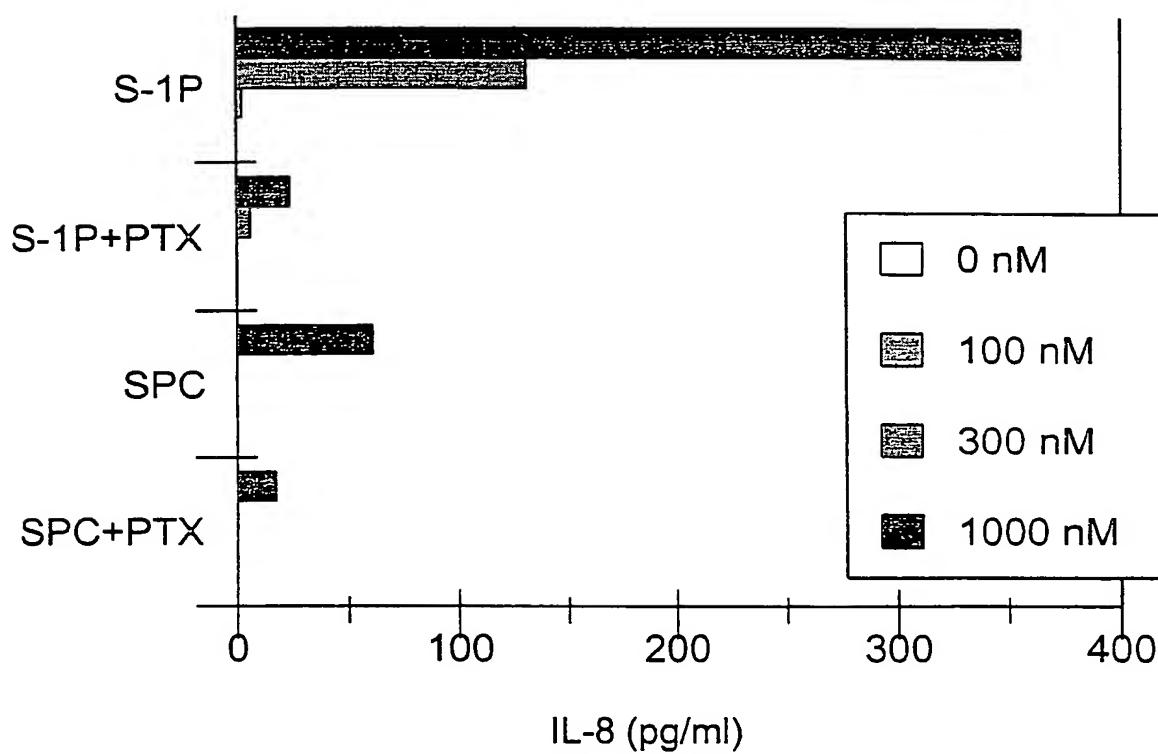


Figure 3.

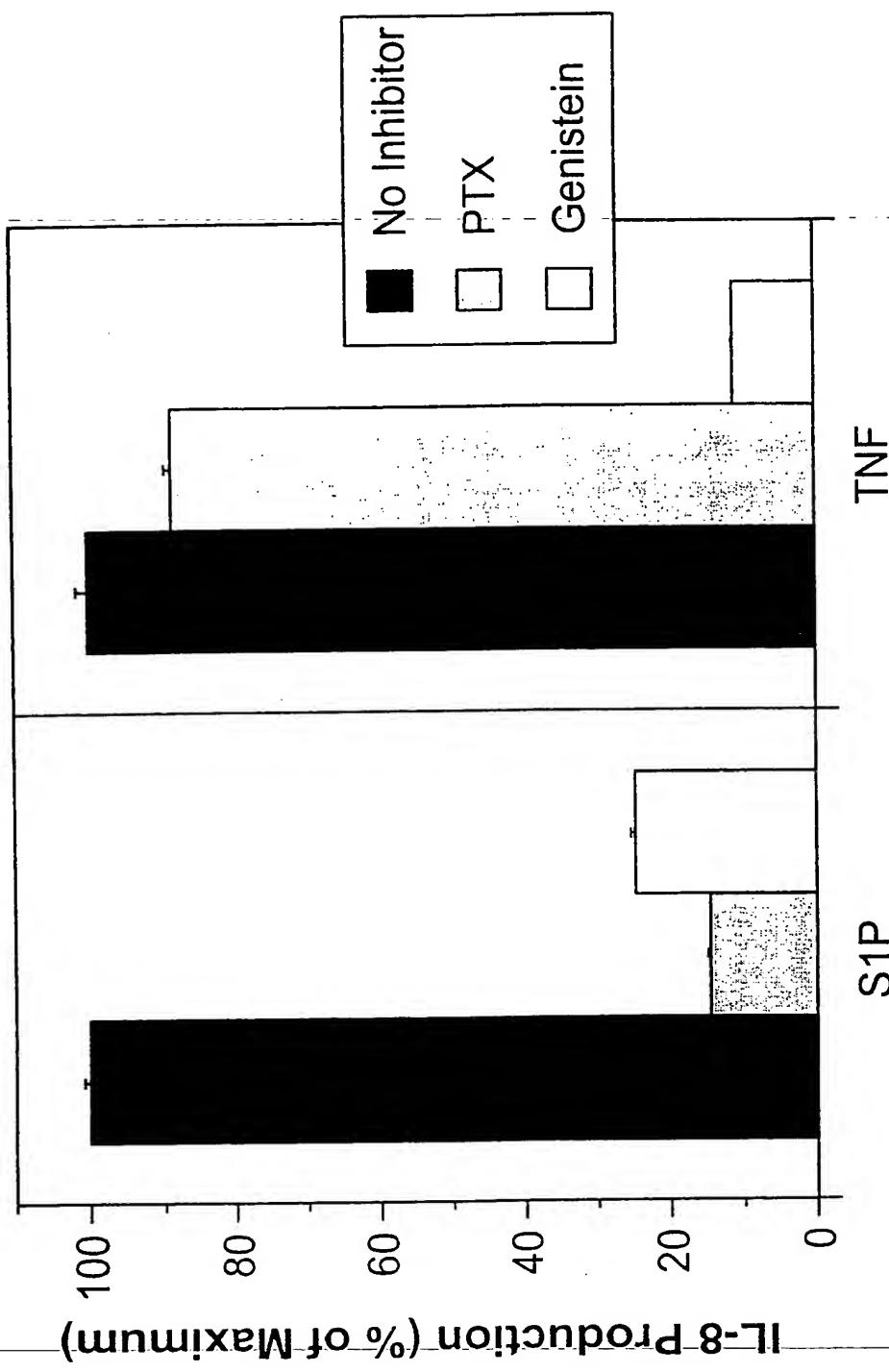


FIGURE 4A

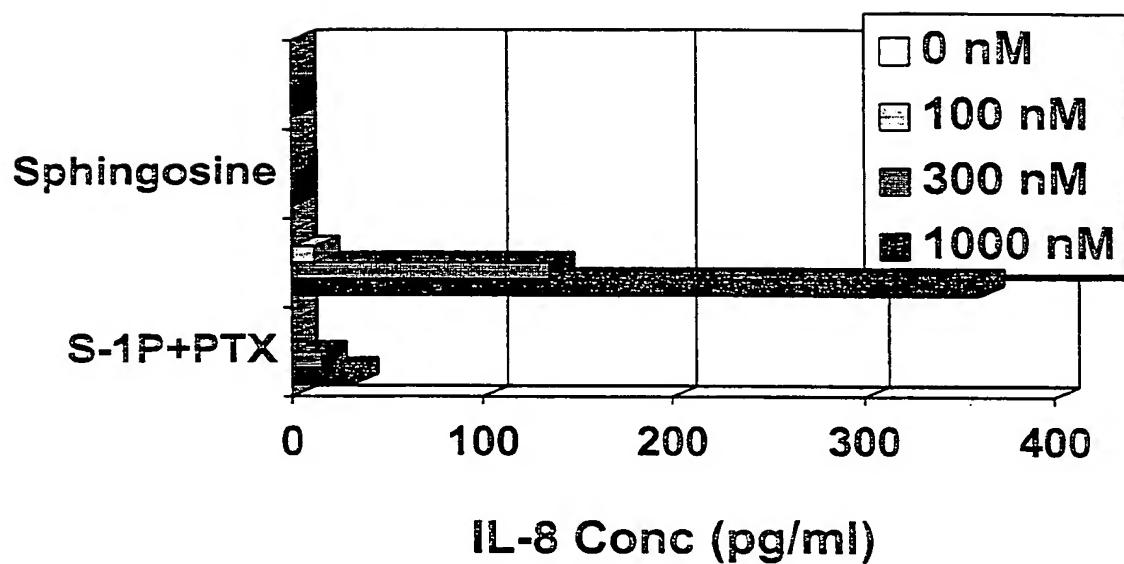


Figure 4B.

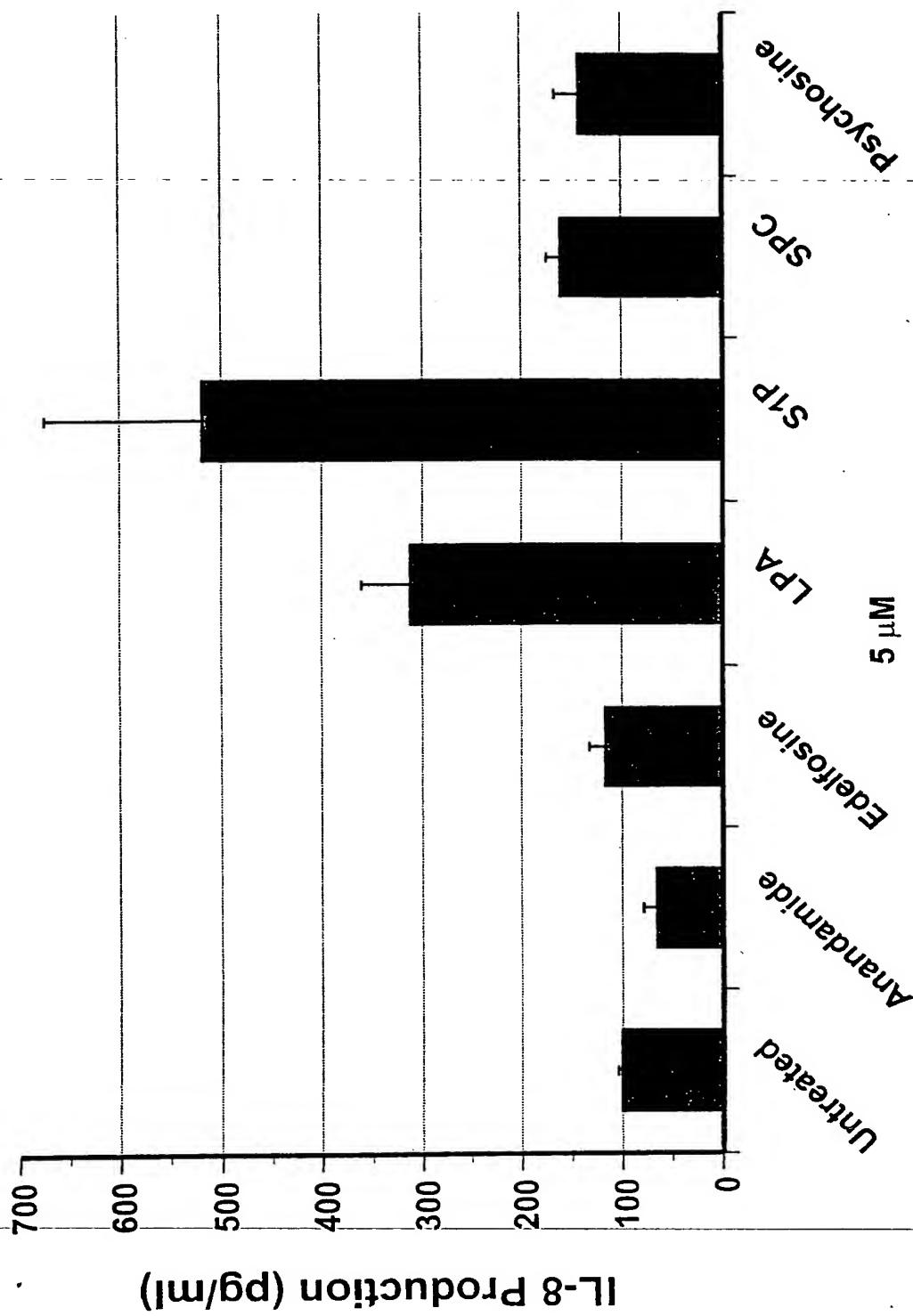
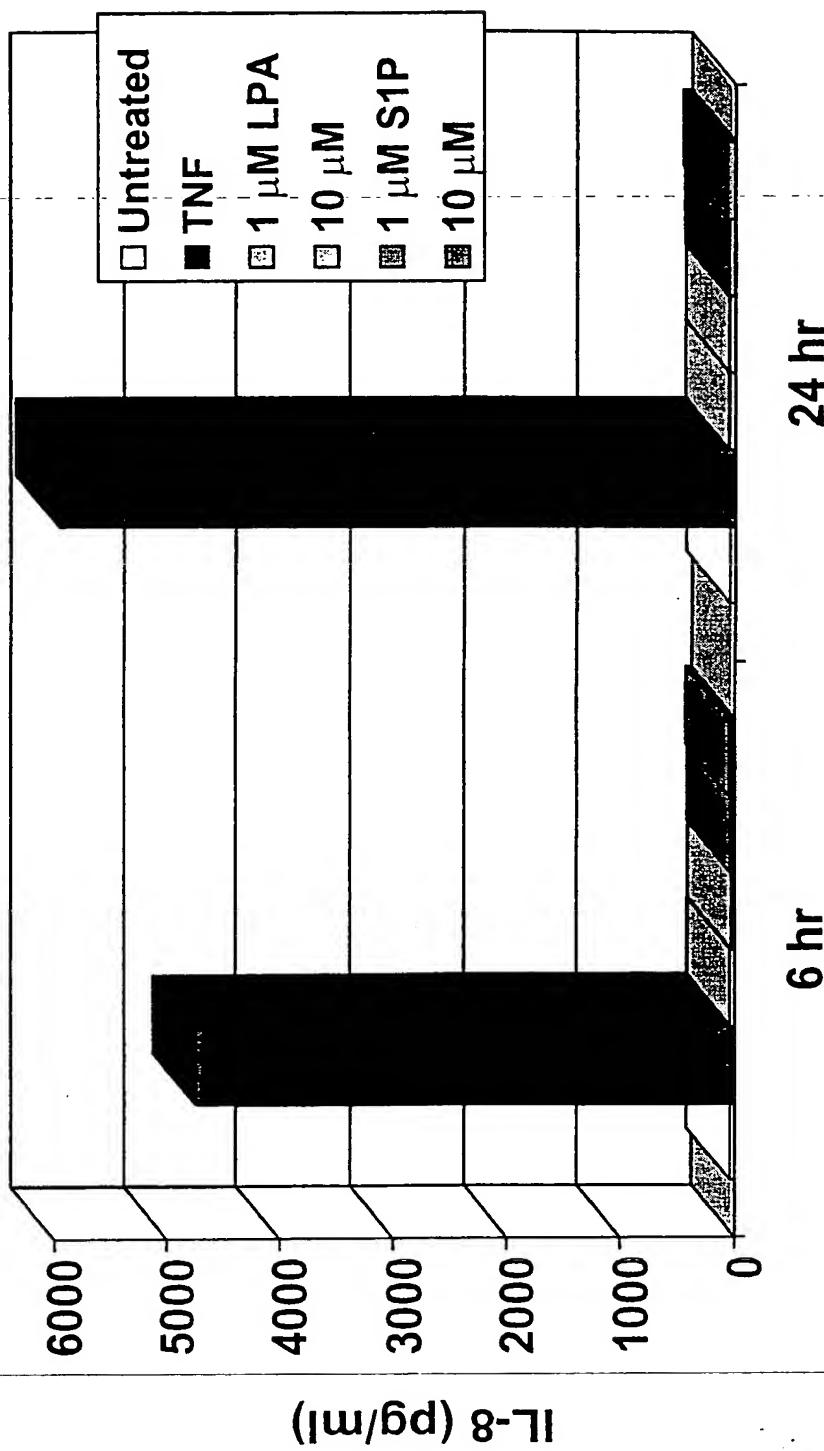


Figure 5.



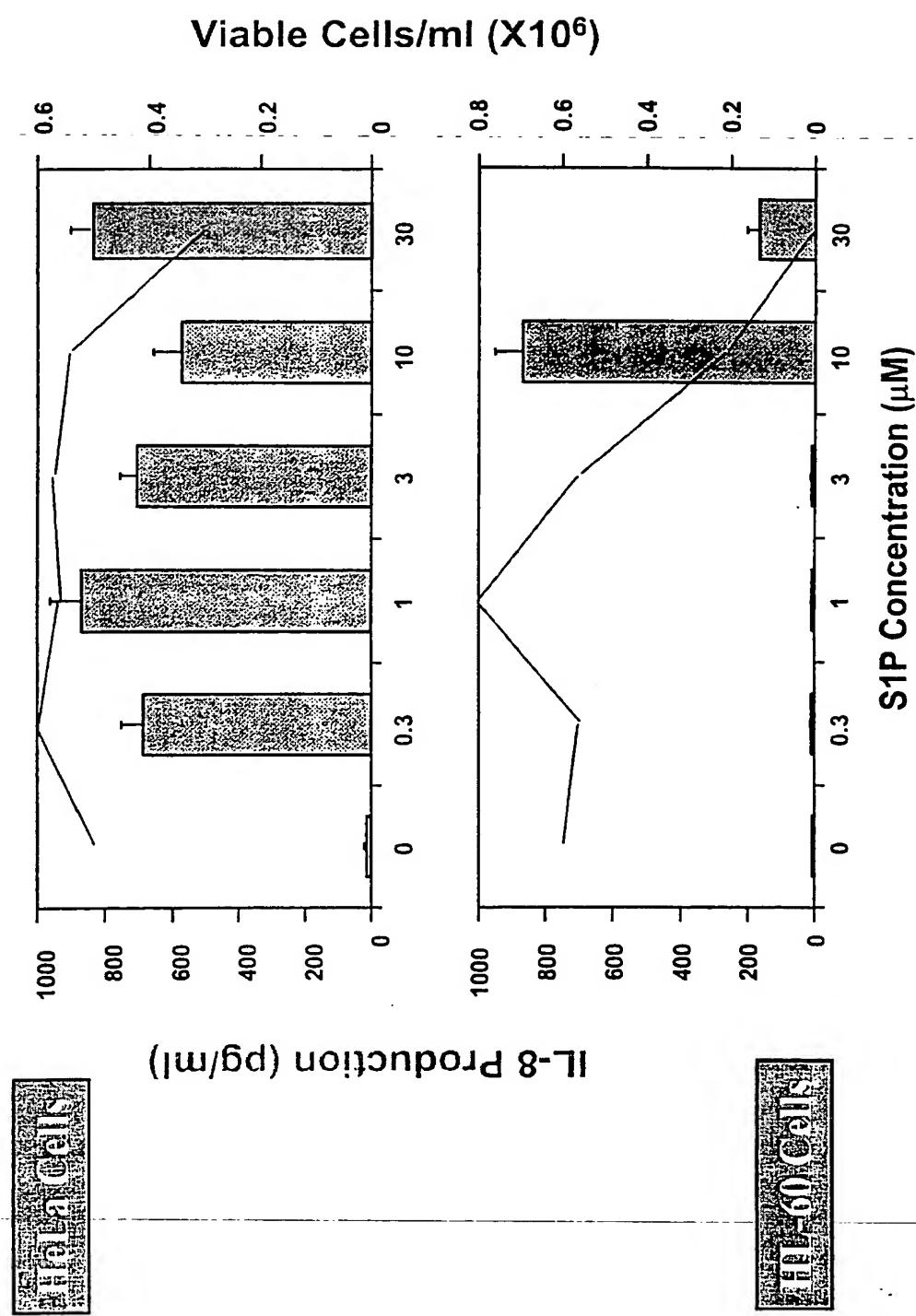


Figure 6.

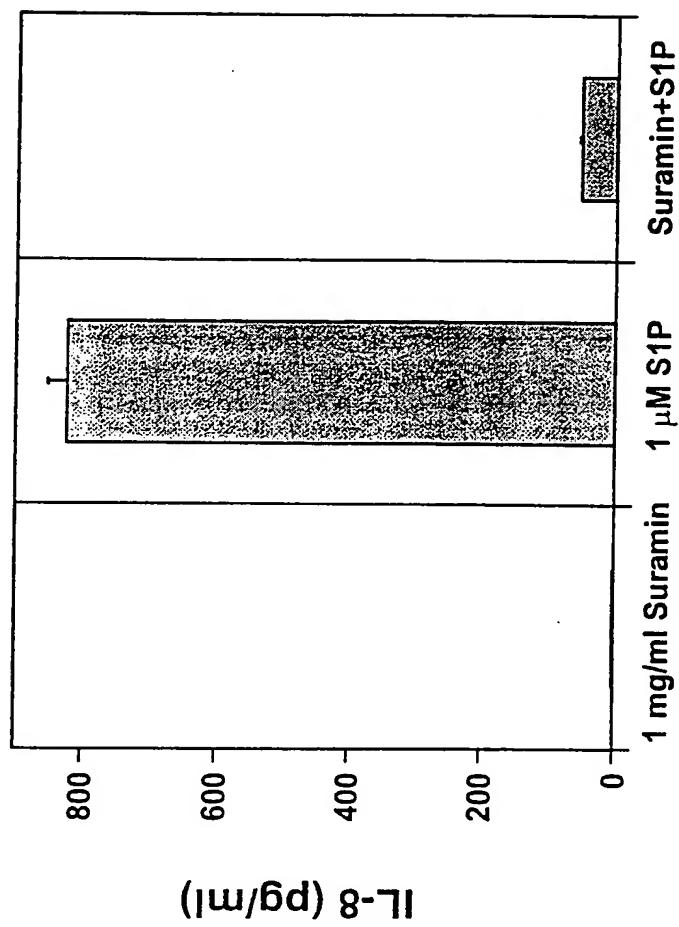


Figure 7.

Figure 8.

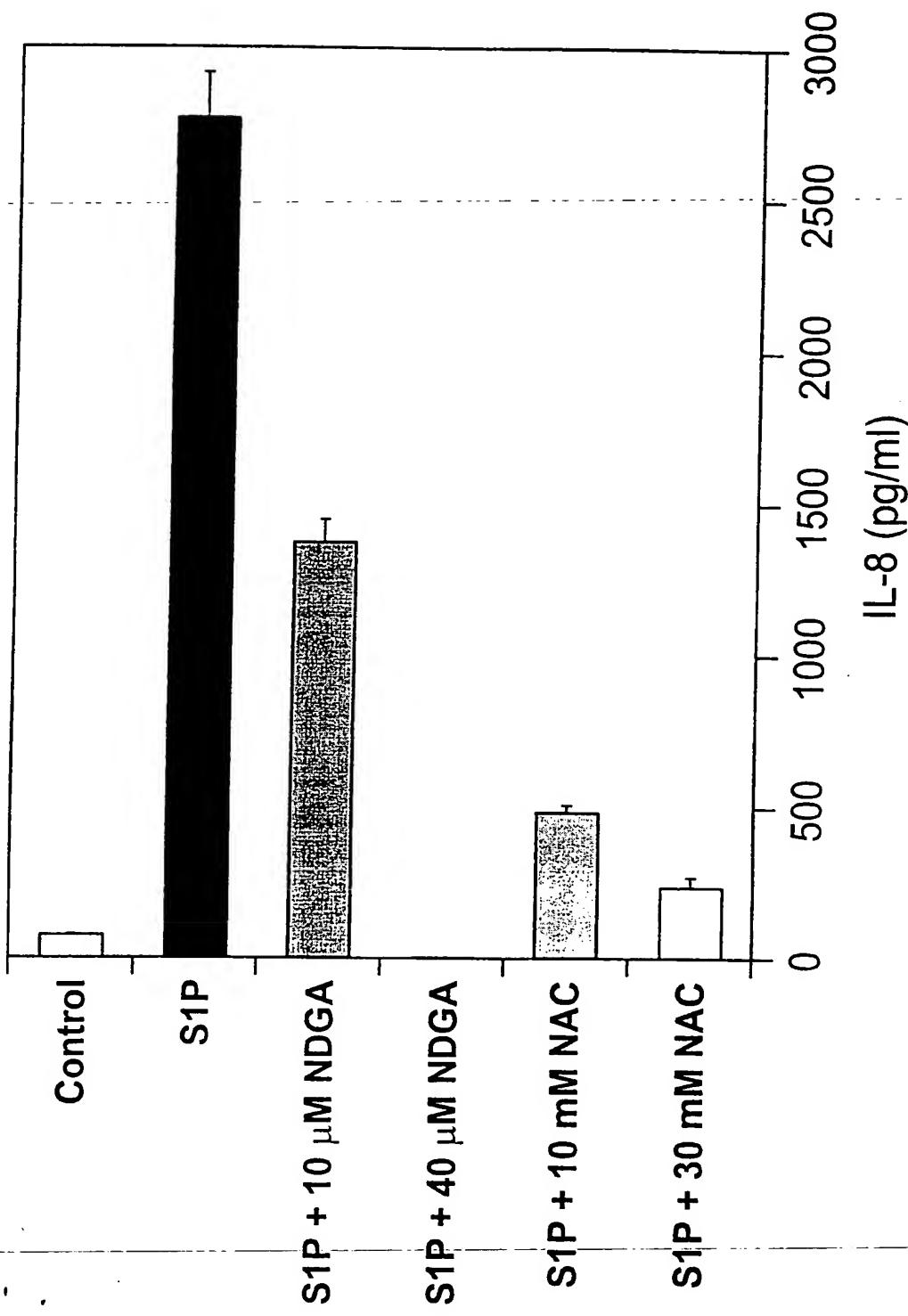


Figure 9.

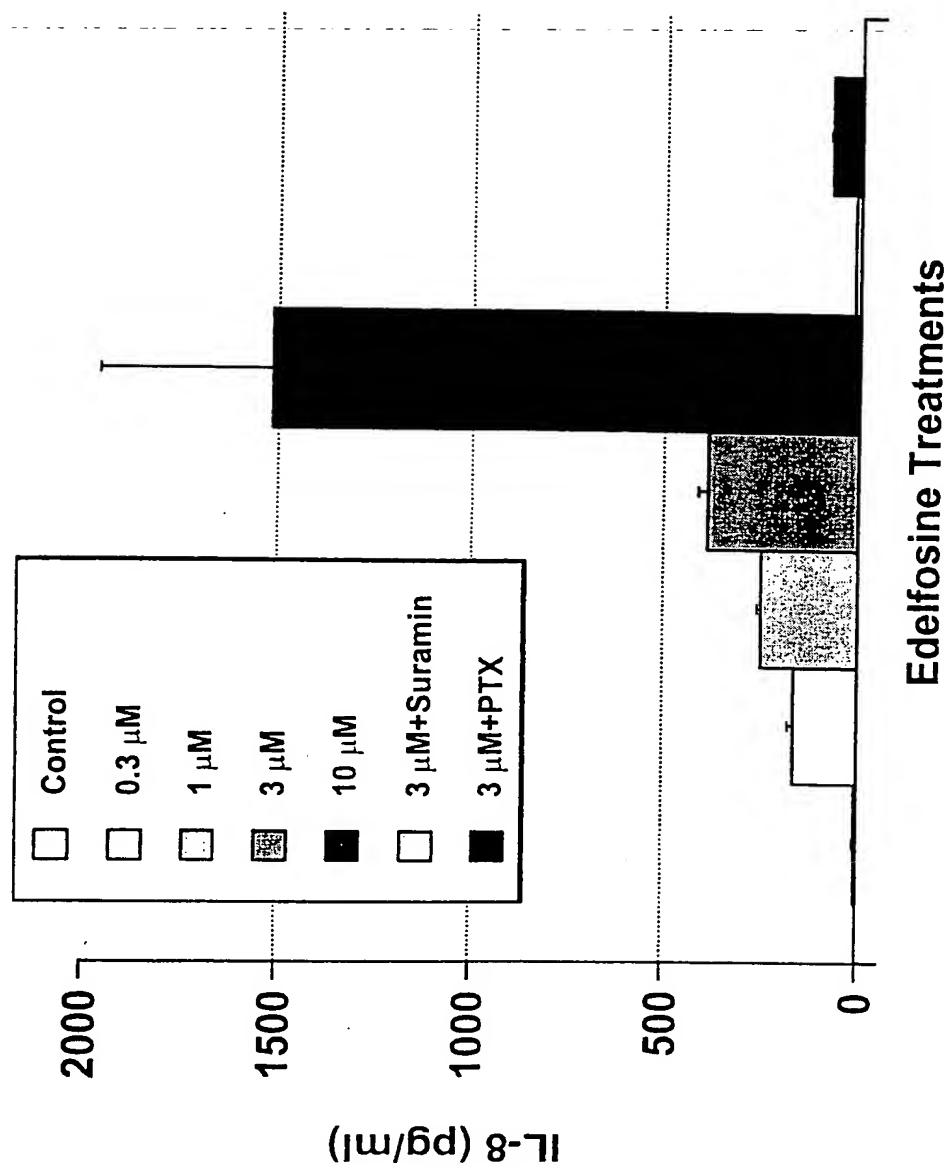


FIGURE 10A

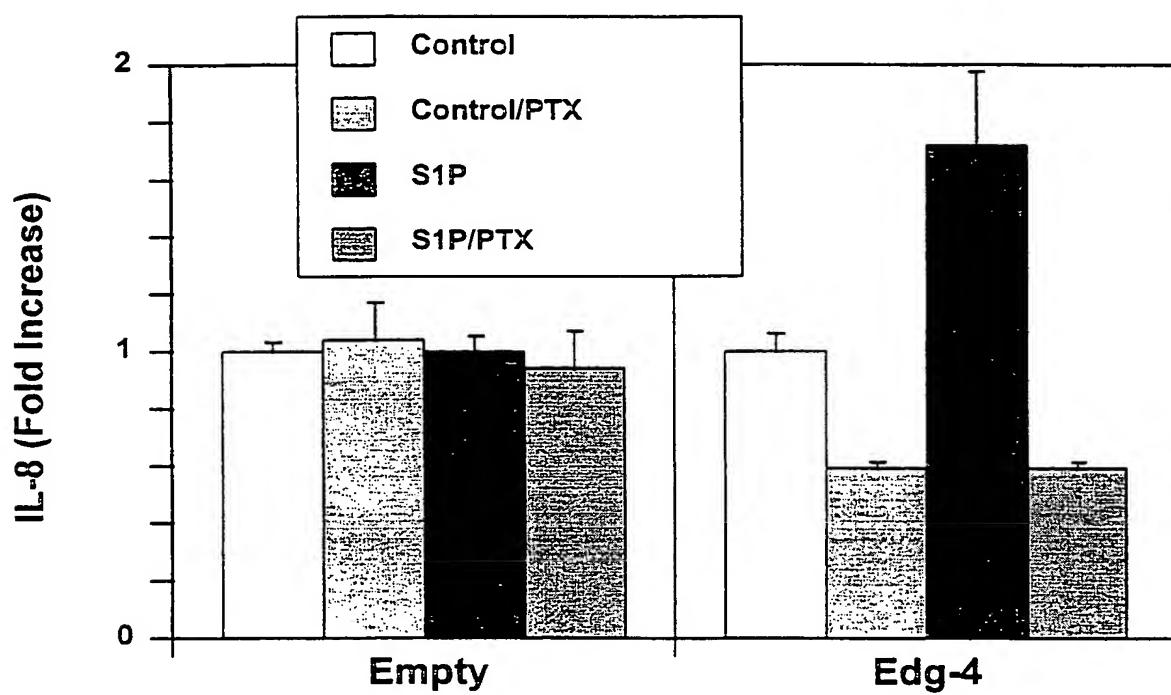


Figure 10B

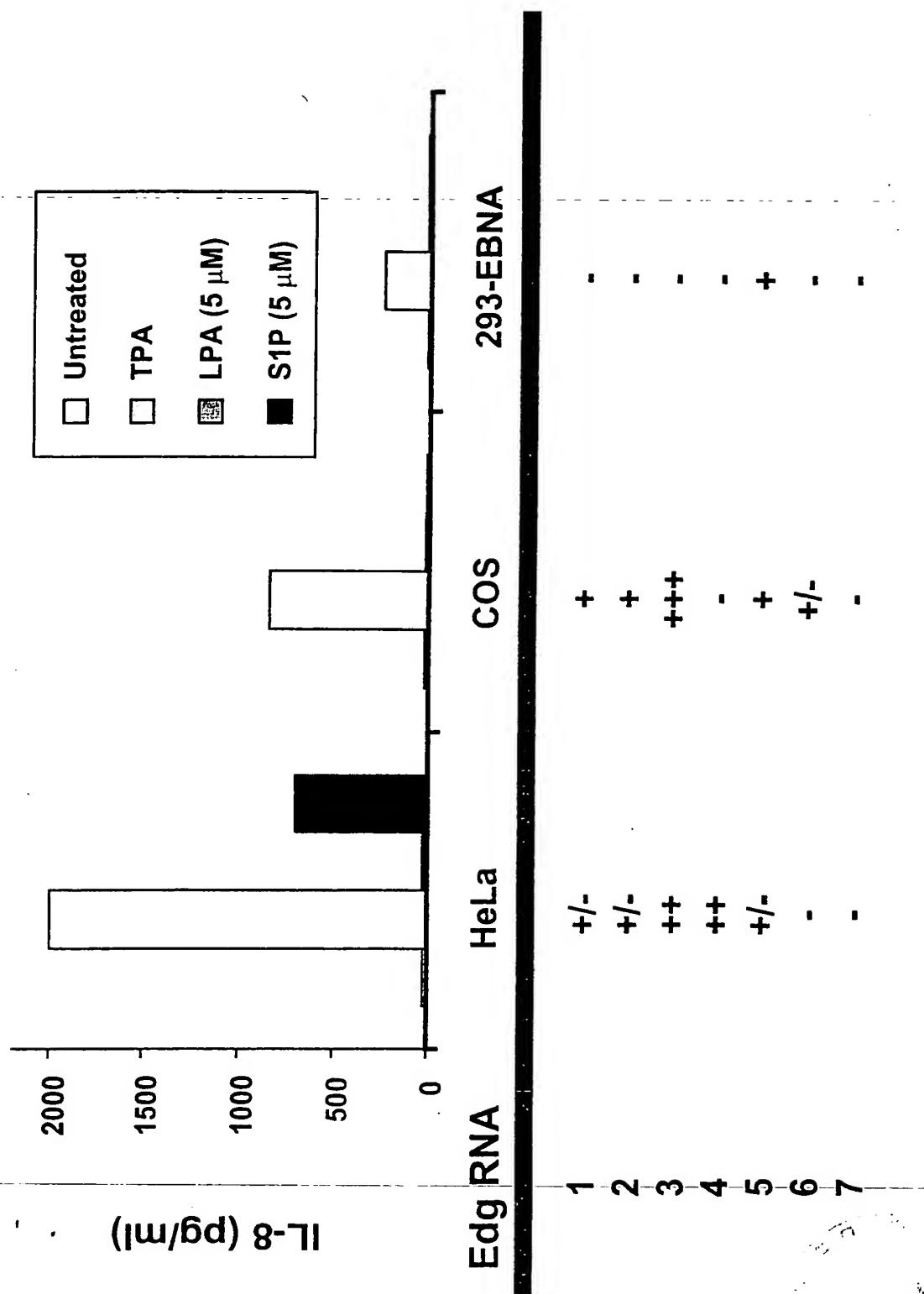


Figure 11.

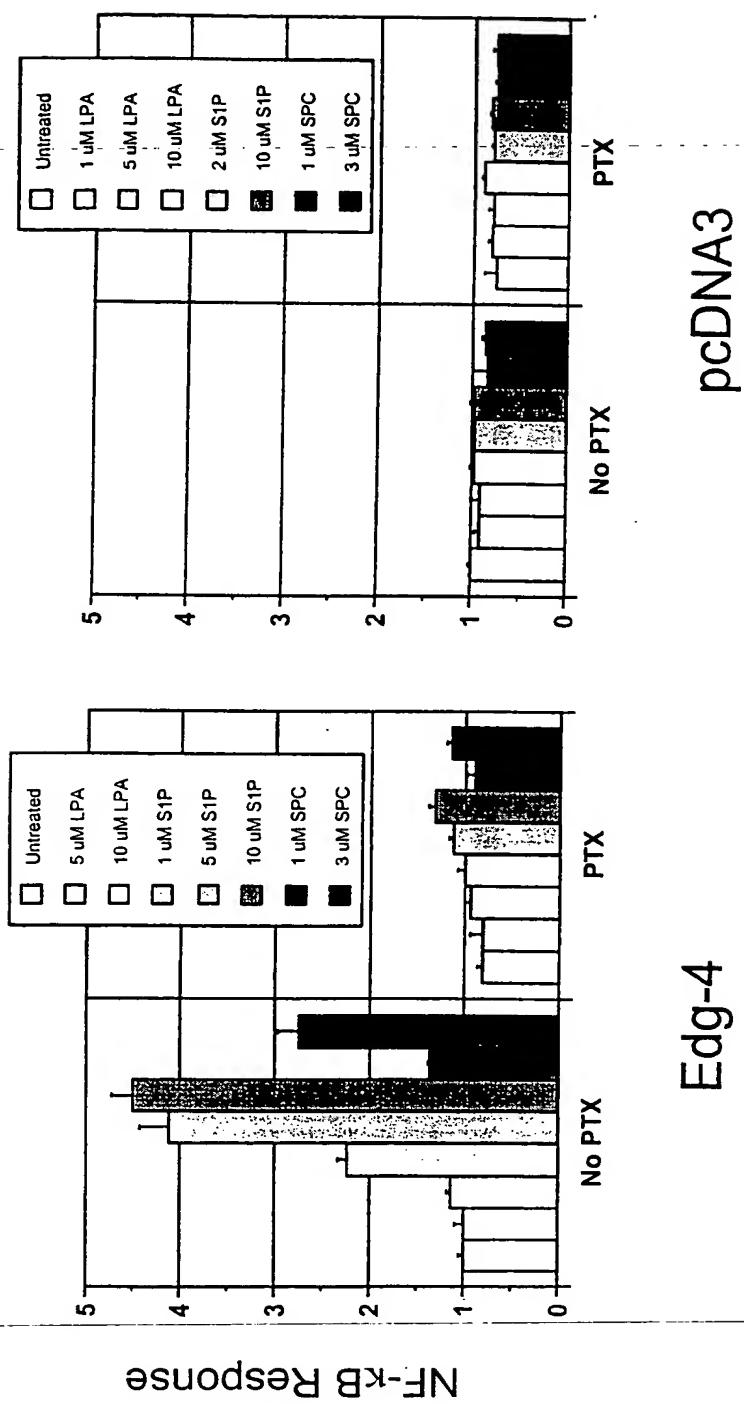


Figure 12.

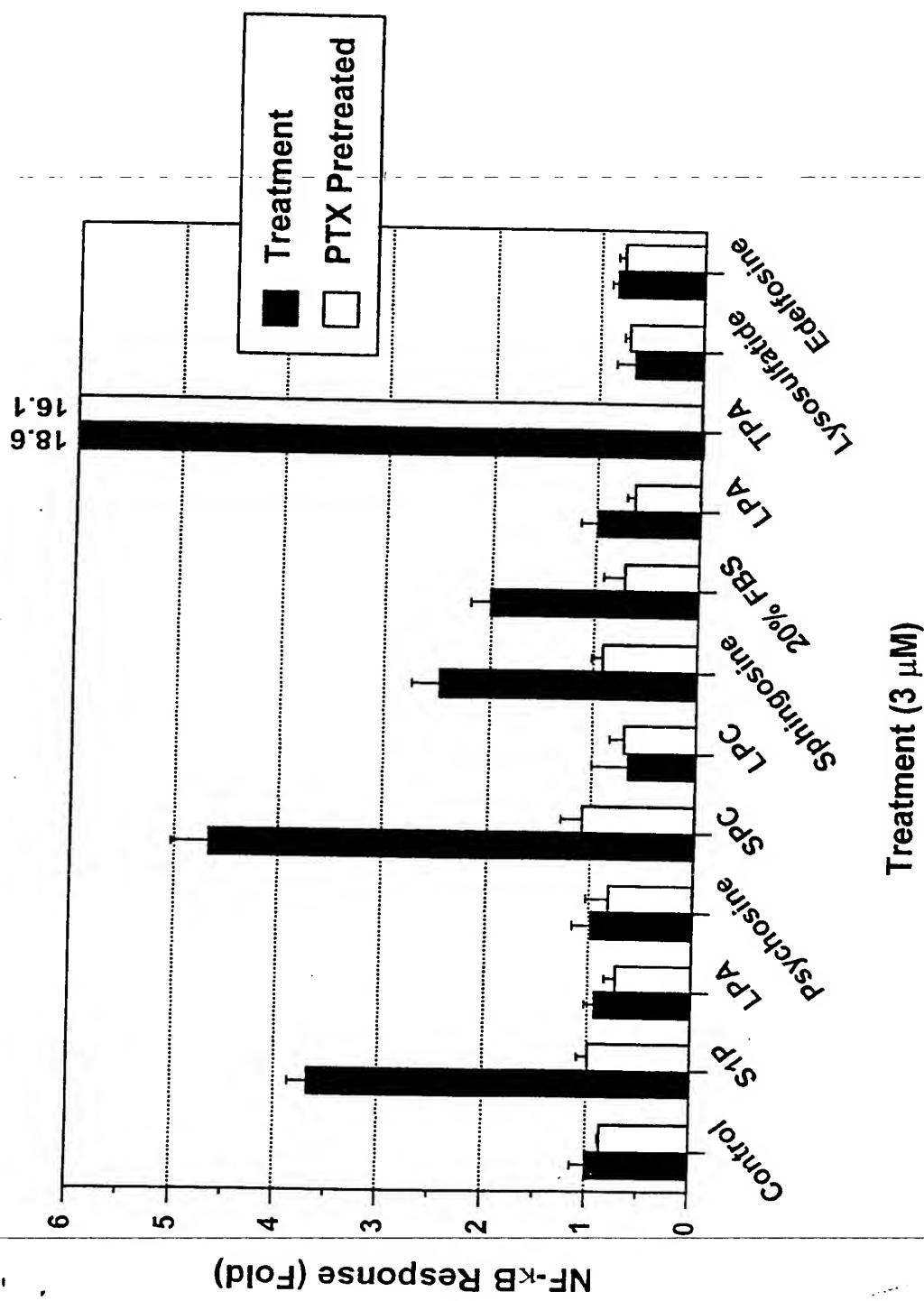


Figure 13.

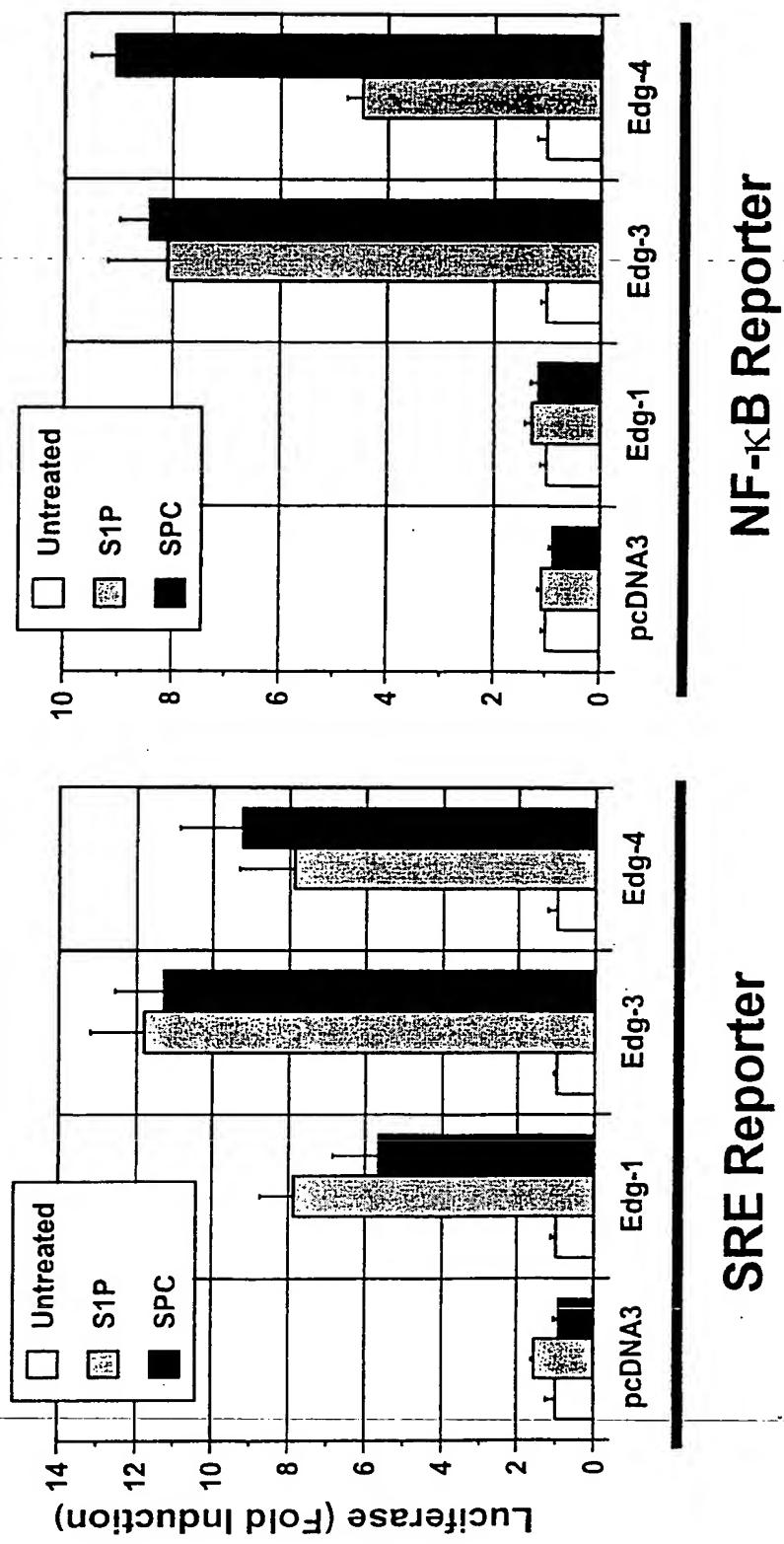


FIGURE 14

1	50
AA834537	-----AAA GCCCCATGGC CCCAGCAGGC CTCTGAGCCC CACCATGGC
AA804628	-----AAA GCCCCATGGC CCCAGCAGGC CTCTGAGCCC CACCATGGC
AA827835	AGTTCTGAAA GCCCCATGGC CCCAGCAGGC CTCTGAGCCC CACCATGGC
51	100
AA834537	AGCTTGTACT CGGAGTACCT GAACCCAAC AAGGTCCAGG AACACTATAA
AA804628	AGCTTGTACT CGGAGTACCT GAACCCAAC AAGGTCCAGG AACACTATAA
AA827835	AGCTTGTACT CGGAGTACCT GAACCCAAC AAGGTCCAGG AACACTATAA
101	150
AA834537	TTATACCAAG GAGACGCTGG AAACGCAGGA GACGACCTCC CGCCAGGTGG
AA804628	TTATACCAAG GAGACGCTGG AAACGCAGGA GACGACCTCC CGCCAGGTGG
AA827835	TTATACCAAG GAGACGCTGG AAACGCAGGA GACGACCTCC CGCCAGGTGG
151	200
AA834537	CCTCGGCATT CATCGTCATC CTCTGTTGCG CCATTGTGGT GGAAACCTT
AA804628	CCTCGGCCTT CATCGTCATC CTCTGTTGCG CCATTGTGGT GGAAACCTT
AA827835	GCTCGGCCTT CATCGTCATC CTCTGTTGCG CCATTGTGGT GGAAACCTT
201	250
AA834537	CTGGTGCTCA TTGCGGTGGC CCGAACACAGC AAGTTCCACT CGGCAATGTA
AA804628	CTGGTGCTCA TTGCGGTGGC CCGAACACAGC AAGTTCCACT CGGCAATGTA
AA827835	CTGGTGCTCA TTGCGGTGGC CCGAACACAGC AAGTTCCACT CGGCAATGTA
251	300
AA834537	CCTGTTCTG GGCAACCTGG CCGCCTCCGA TCTACTGGCA GGCGTGGCCT
AA804628	CCTGTTCTG GGCAACCTGG CCGCCTCCGA TCTACTGGCA GGCGTGGCCT
AA827835	CCTGTTCTG GGCAACCTGG CCGCCTCCGA TCTACTGGCA GGCGTGG.CT
301	350
AA834537	TCGTAGCCAA TACTTGCTC TCTGGCTCTG TCACGCTGAG GCTGACGCCT
AA804628	TCGTAGCCAA TACTTGCTC TCTGGCTCTG TCACGCTGAG GCTGACGCCT
AA827835	TCGTAGCCAA TACTTGCTC TCTGGCTCTG TCACGCTGAG GCTGACGCCT
351	400
AA834537	GTGCAGTGGT TTGCCCCGGGA CGGTCTGCCT TCATCACGCT CTCGGCTCT
AA804628	GTGCAGTGGT TTGCCCCGGGA C----- -----
AA827835	GTGCAGTGGT TTGCCCCGGGA ----- -----
401	450
AA834537	GTCTTCAGCC TCCTGGCCAT CGCCATTGAG CGCCACGTGG CCATTGCAA
AA804628	----- ----- ----- -----
AA827835	----- ----- ----- -----
451	
AA834537	GG
AA804628	--
AA827835	--

FIGURE 15 A

M G S L Y S E Y  
 1 AAAGCCCCATGGCCCCAGCAGGCCTCTGAGCCCACCATGGCAGCTGTACTCGGAGTA 60  
 TTTGGGGTACCGGGTCTGGAGACTCGGGTGGTACCCGTCGAACATGAGCCTCAT  
 L N P N K V Q E H Y N Y T K E T L E T Q  
 CCTGAACCCAAACAAGGTCCAGGAACACTATAATTACCAAGGAGACGCTGGAAACGCA 120  
 61 GGACTTGGGTTGTTCCAGGTCTTGTGATATTAAATGGTTCTCTGCGACCTTGCGT  
 E T T S R Q V A S A F I V I L C C A I V  
 GGAGACGACCTCCGCCAGGTGGCCTCGCCTCATCGTCATCCTCTGTCGCGCCATTGT 180  
 121 CCTCTGCTGGAGGGCGGTCCACCGGAGCCGAAGTAGCAGTAGGAGACAACGCGTAACA  
 V E N L L V L I A V A R N S K F H S A M  
 GGTGGAAAACCTCTGGTGTCTGGCCTCGATCTACTGGCAGGGGTGGCCACTCGGCAAT 240  
 181 CCACCTTTGGAAGACACGAGTAACGCCACCGGGCTTGTGTTCAAGGTGAGCCGTTA  
 Y L F L G N L A A S D L L A G V A F V A  
 GTACCTGTTCTGGCAACCTGGCCGCTCCGATCTACTGGCAGGGGTGGCCCTCGTAGC 300  
 241 CATGGACAAAGACCCGTTGGACCGGGAGGCTAGATGACCGTCCGCACCGGAAGCATCG  
 N T L L S G S V T L R L T P V Q W F A R  
 CAATAACCTTGTCTCTGGCTCTGTACGCTGAGGCTGACGCCGTGCACTGGTTGCCCG 360  
 301 GTTATGGAACGAGAGACCGAGACAGTGCAGACTCCGACTGCGAACACGTCAACAAACGGC  
 E G S A F I T L S A S V F S L L A I A I  
 GGAGGGCTCTGCCCTCATCACGCTCTGGCTCTGTCTTCAGCCTCTGGCATTGCCAT 420  
 361 CCTCCGAGACGGAAGTAGTGCAGAGCCGGAGACAGAAGTCGGAGGACCGGTAGCGGT  
 E R H V A I A K V K L Y G S D K S C R M  
 TGAGGCCACGTGGCATTGCCAAGGTCAAGCTGTATGGCAGCGACAAGAGACTGCCAT 480  
 421 ACTCGCGGTGCACCGTAACGGTCCAGTTGACATACCGTCGCTGTTCTGACGGCGTA  
 L L L I G A S W L I S L V L G G L P I L  
 GCTTCTGCTCATGGGGCCTCGTGGCTCATCTCGCTGGCTCGGTGGCCATCCT 540  
 481 CGAAGACGAGTAGCCCCGGAGCACCAGTAGAGCGACCGAGGAGCCACCGGACGGTAGGA  
 G W N C L G H L E A C S T V L P L Y A K  
 TGGCTGAACTGCCCTGGCACCTCGAGGCCTGCTCCACTGTCTGCCTCTACGCCAA 600  
 541 ACCGACCTTGACGGACCCGGTGGAGCTCCGGACGAGGTGACAGGAGGAGATGCGGTT  
 H Y V L C V V T I F S I I L L A I V A L  
 GCATTATGTGCTGTGCGTGGTGACCATCTCTCCATCATCCTGTTGGCCATCGTGGCCCT 660  
 601 CGTAATACACGACACGCACCACTGGTAGAAGAGGTAGTAGGACAACCGTAGCACCAGGA

Y V R I Y C V V R S S H A D M A A P Q T  
 GTACGTGCGCATCTACTGCGTGGTCCGCTCAAGCCACGCTGACATGGCCGCCCGCAGAC  
 661 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CATGCACGCGTAGATGACGCACCAGGCAGTTGGTGCAGCTGTACCGCGGGCGTCTG  
 720

L A L L K T V T I V L G V F I V C W L P  
 GCTAGCCCTGCTCAAGACGGTACCATCGTCTAGGGCTCTTATCGTCTGGCTGCC  
 721 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CGATCGGGACGAGTTCTGCCAGTGGTAGCACGATCCGAGAAATAGCAGACGACCGACGG  
 780

A F S I L L D Y A C P V H S C P I L Y  
 CGCCTTCAGCATCCTCCTCTGGACTATGCCGTCCACTCCTGCCGATCCTCTA  
 781 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 GCGGAAGTCGTAGGAGGAAGACCTGATAACGGACAGGGCAGGTGAGGACGGCTAGGAGAT  
 840

K A H Y X F A V S T L N S L L N P V I Y  
 CAAAGCCCACACTACYTTTCGCCGTCTCACCCCTGAATTCCCTGCTCAACCCCGTCATCTA  
 841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 GTTCGGGTGATGRAAAAGCGGCAGAGGTGGACTTAAGGGACGAGTTGGGCAGTAGAT  
 900

T W R S R D L R R E V L R P L Q C W R P  
 CACGTGGCGCAGCCGGGACCTGCGGGAGGTGCTCGGCCGTGAGTGCAGTGCCTGGCG  
 901 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 GTGCACCGCGTCGGCCCTGGACGCCCTCACGAAGCCGGGACGTNACGACCGCCGG  
 960

G V G V Q G R R R G G T P G H H L L P L  
 GGGGGTGGGGGTGCAAGGACGGAGGGCGGGACCCCGGGCACCCACCTGCCACT  
 961 -----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CCCCCACCCCCACGTTCTGCCCTCGCCCCGCCCTGGGCCCCGGTGGAGGACGGTGA  
 1020

R S S S L E R G M H M P T S P T F L E  
 CCGCAGCTCCAGCTCCCTGGAGAGGGCATGCACATGCCACGTACCCACGTTCTGGA  
 1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+  
 GGCCTCGAGGTGAGGGACCTCTCCCCGTACGTGTACGGGTGCAGTGGGTGAAAAGACCT  
 1080

G N T V V \*

GGGCAACACGGTGGTCTGAGGGTGGGGTGGACCAACAACCAGGCCAGGGCATAGGGTT  
 1081 -----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CCCGTTGTGCCACCACTCCACCCACCTGGTGTGGTCCGGTCCCGTATCCCCAA  
 1140

CATGGAAAGGCCACTGGGTGACCCAAATA  
 1141 -----+-----+-----+-----+-----+-----+-----+-----+-----+  
 GTACCTTCCGGTGACCCACTGGGTTTAT 1170

**Figure 15B****cDNA sequence of clone pC3-hedg4#36 encoding functional HEDG4 receptor protein.**

1	ATGGGCAGCTTGTACTCGGAGTACCTGAACCCCAACAAGGTCCAGGAACACTATAATTAT	60
	TACCCGTCGAACATGAGCCTCATGGACTGGGGTTGTTCCAGGTCTTGTGATATTAATA	
61	ACCAAGGAGACGCTGGAAACGCAGGAGACGACCTCCGCCAGGTGGCCTCGGCCTTCATC	120
	TGGTTCCCTCTGCGACCTTGCGTCCTCTGCTGGAGGGCGGTCCACCGGAGCCGGAAGTAG	
121	GTCATCCTCTGTTGCCATTGTGGTGGAAAACCTTCTGGTGTCAATTGGGTGGCCGA	180
	CAGTAGGAGACAACGCCGTTAACACCACCTTGGAAGACCACGAGTAACGCCACCGGGCT	
181	AACAGCAAGTCCACTCGGCAATGTACCTGTTCTGGCAACCTGGCCGCCTCCGATCTA	240
	TTGTCGTTCAAGGTGAGCCGTTACATGGACAAAGACCCGTTGGACCGGGGAGGCTAGAT	
241	CTGGCAGGCGTGGCCTTCGTAGCCAATACCTTGCTCTGGCTCTGTCACGCTGAGGCTG	300
	GACCGTCCGACCGGAAGCATCGTTATGGAACGAGAGACCGAGACAGTGCAGTCCGAC	
301	ACGCCTGTGAGTGGTTGCCGGAGGGCTCTGCCTTCATCACGCTCTGGCCTCTGTC	360
	TGCGGACACGTCACCAAACGGGCCCTCCGAGACGGAAGTAGTGCAGAGACAGCGGAGACAG	
361	TTCAGCCTCTGCCATGCCATTGAGGCCACGTGGCATTGCCAAGGTCAAGCTGTAT	420
	AAGTCGGAGGACCGGTAGCGGTAACTCGCGGTGACCGGTAACGGTTCCAGTCGACATA	
421	GGCAGCGACAAGAGCTGCCATGCTTCATCGGGCCTCGTGGCTCATCTCGCTG	480
	CCGTCGCTGTTCTGACGGCGTACGAAGACGAGTAGCCCCGGAGCACCAGTAGAGCGAC	
481	GTCCTCGGTGGCCTGCCCATCCTGGCTGGAACCTGCCTGGCCACCTCGAGGCCTGCTCC	540
	CAGGAGCCACCGGACGGTAGGAACCGACCTTGACGGACCCGGTGGAGCTCCGGACGAGG	
541	ACTGTCCTGCCTCTACGCCAAGCATTATGTGCTGTGCGTGGTGAACATCTTCTCCATC	600
	TGACAGGACGGAGAGATGCGGTTGTAATACACGACACGCACCACTGGTAGAAGAGGTAG	
601	ATCCTGTTGCCGTCGTGGCCCTGTACGTGCGCATCTACTGCGTGGTCCGCTCAAGGCCAC	660
	TAGGACAACCGGCAGCACGGGACATGCAACGCGTAGATGACGCACCAAGGGCAGTTCGGTG	
661	GCTGACATGGCCGCCCGCAGACGCTAGCCCTGCTCAAGACGGTCACCATCGTGCTAGGC	720
	CGACTGTACCGGGGGCGTCTGCGATCGGACGAGTTCTGCCAGTGGTAGCACGATCCG	
721	GTCTTTATCGTCTGCTGGCTGCCGCCCTCAGCATCCTCCTCTGGACTATGCCTGTCCC	780

	CAGAAATAGCAGACGACCGACGGCGGAAGTCGTAGGAGGAAGACCTGATA CGGACAGGG	
781	GTCCACTCCTGCCGATCTACAAAGCCCAC TACCTTTGCCGTCTCCACCCCTGAAT CAGGTGAGGACGGCTAGGAGATGTTCGGGTGATGGAAAAGCGGCAGAGGTGGACTTA	840
841	TCCCTGCTCAACCCCGTCATCTACACGTGGCGAGCCGGACCTGCCGGGGAGGTGCTT AGGGACGAGTTGGGGCAGTAGATGTGCACCGCGTCGGCCCTGGACGCCGCCCTCACGAA	900
901	CGGCCGCTGCAGTGCCTGGCGGCCGGGGTGGGGTGCAAGGACGGAGGCCGGCGGGACC GCCGGCGACGTACGACCGCCGGCCCCACCCCCACGTTCTGCCCTCCGCCCTGG	960
961	CCGGGCCACCACCTCCTGCCACTCCGCA GCTCCAGCTCCCTGGAGAGGGCATGCACATG GGCCCGGTGGTGGAGGACGGTGAGGC GTCGAGGTGAGGGACCTCTCCCCGTACGTGTAC	1020
1021	CCCACGTACCCACGTTCTGGAGGGCAACACGGTGGTCTGA GGGTGCAGTGGGTGAAAGACCTCCCGTTGTGCCCCACCACT	1062

## FIGURE 16 Å

1 MGSLYSEYLN PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIIVVE  
 51 NLLVLIavar NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL  
 101 TPVQWFAREG SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL  
 151 LIGASWLISL VLGGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI  
 201 ILLAIVALYV RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPF  
 251 SILLLDYACP VHSCPILYKA HYXFAVSTLN SLLNPVIYTW RSRDLRREVL  
 301 RPLQCWRPGV GVQGRRGGT PGHHLLPLRS SSSLERGMHM PTSPTFLEGN  
 351 TVV\*

Conserved features of G-protein coupled receptors include:

N-terminal extracellular domain:	Residues 1 - 36
TM-I:	Residues 37 - 57
Intracellular loop 1:	Residues 58 - 68
TM-II:	Residues 69 - 92
Extracellular loop 1:	Residues 93 - 111
TM-III:	Residues 112 - 130
Intracellular loop 2:	Residues 131 - 149
TM-IV:	Residues 150 - 168
Extracellular loop 2:	Residues 169 - 185
TM-V:	Residues 186 - 210
Intracellular loop 3:	Residues 211 - 232
TM-VI:	Residues 233 - 254
Extracellular loop 3:	Residues 255 - 266
TM-VII:	Residues 267 - 285
C-terminal cytoplasmic domain:	Residues 286 - 353

Potential post-transcriptional modification sites:

N-glycosylation:	Residues 19
Phosphorylation:	Residues 142, 145, 219, 289, 332, 345
Myristylation:	Residues 141, 318

**Figure 16B****Predicted amino acid sequence of HEDG4 polypeptide encoded by pC3-hedg4#36.**

1 MGSLYSEYLN PNKVQEHYN Y TKETLETQET TSRQVASAFI VILCCAIIVVE

51 NLLVLIAVAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL

101 TPVQWFAREG SAFITLSASV FSLLAIAIER HVAIAKVLY GSDKSCRMLL

151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI

201 ILLAVVALYV RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPF

251 SILLLDYACP VHSCPILYKA HYLFAVSTLN SLLNPVIYT W RSRDLRREVL

301 RPLQCWRPGV GVQGRRGGT PGHHLLPLRS SSSLERGMHM PTSPTFLEG N

351 TVV

## FIGURE 17 A

Human	1 MGSLYSEYLNPNKVQEHYNYTKE <del>T</del> LETQETTSRQVASAFIVILCCAI <del>V</del> E 50
Rat	1 MGGLYSEYLNP <del>E</del> KVQEHYNYTKE <del>T</del> LDMQETPSRKVASAFIIILCCAI <del>V</del> E 50
Human	51 NLLVLI <del>A</del> VARNSKFHSAMYLFLGNLAASD <del>L</del> LAGVAFVANTLLSGV <del>T</del> RL 100
Rat	51 NLLVLI <del>A</del> VARNSKFHSAMYLFLGNLAASD <del>L</del> LAGVAFVANTLLSGPVT <del>L</del> SL 100
Human	101 TPVQWFAREGSAF <del>I</del> TSASVF <del>S</del> LLAIAIERHVAIAKVKLYGSDKSCRML <del>L</del> 150
Rat	101 TPLQWFAREGSAF <del>I</del> TSASVF <del>S</del> LLAIAIERQVAIAKVKLYGSDKSCRML <del>M</del> 150
Human	151 LIGASWLISLVLGG <del>L</del> PILGW <del>N</del> CLGHLEAC <del>S</del> T <del>V</del> LPLYAKHYVLCVVTIFSI 200
Rat	151 LIGASWLISL <del>L</del> GG <del>L</del> PILGW <del>N</del> CLDHLEAC <del>S</del> T <del>V</del> LPLYAKHYVLCVVTIFSV 200
Human	201 ILLAIVALYVRIYCVVRSSHADMAAPQ <del>T</del> LALLKT <del>V</del> TIVLGV <del>F</del> IVCWLP <del>A</del> F 250
Rat	201 ILLAIVALYVRIYFVVRSSHADVAGP <del>Q</del> TLALLKT <del>V</del> TIVLGV <del>F</del> IICWLP <del>A</del> F 250
Human	251 SILL <del>D</del> YACP <del>V</del> HSCPILYKAHYXFAV <del>S</del> TLNSLLNPVIYT <del>W</del> RSRDLRREVL 300
Rat	251 SILL <del>D</del> STCPVRACP <del>V</del> LYKAHYFFAFATLNSLLNPVIYT <del>W</del> RSRDLRREVL 300
Human	301 RPLQCWRPGVG <del>V</del> QGR <del>R</del> GGTPGH <del>H</del> LLPLR <del>S</del> SSSLERGMHMPTSPTFLEG <del>N</del> 350
Rat	301 RPLLCWRQGKGATG.RRGGNP <del>G</del> H <del>R</del> LLPLR <del>S</del> SSSLERGLHMPTSPTFLEG <del>N</del> 349
Human	351 TVV* 353
Rat	350 TVV* 352

Figure 17B

**Alignment of HEDG4 with pC3-hedg4#36 translation product and rat H218 (REDG4).** Differences between pC3-hedg4#36 translation product and previously determined HEDG4 polypeptide are indicated in reverse text. Differences between rat and human edg-4 polypeptide sequences are shown in bold, shaded text.

1	50
HEDG4	MGS <del>LYSE</del> YLN PNKVQE <del>HY</del> NY TKETLETQET TSRQVASAFI VILCCAI <del>V</del> V
HEDG4#36	MGS <del>LYSE</del> YLN PNKVQE <del>HY</del> NY TKETLETQET TSRQVASAFI VILCCAI <del>V</del> V
REDG4	MG <del>G</del> LYSE <del>Y</del> LN PEKVQE <del>HY</del> NY TKET <del>L</del> <u>D</u> MQET <del>RSR</del> <b>K</b> VASAFI <del>V</del> I <del>L</del> CCAI <del>V</del> V
51	100
HEDG4	NLLVLI <del>A</del> VAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
HEDG4#36	NLLVLI <del>A</del> VAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
REDG4	NLLVLI <del>A</del> VAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSG <del>E</del> VTL <del>S</del> L
101	150
HEDG4	TPVQWFAREG SAFITLSASV FSLLAIAIAIER HVAIAKV <del>K</del> LY GSDKSCRMLL
HEDG4#36	TPVQWFAREG SAFITLSASV FSLLAIAIAIER HVAIAKV <del>K</del> LY GSDKSCRMLL
REDG4	TP <del>T</del> QWFAREG SAFITLSASV FSLLAIAIAIER QVVAIAKV <del>K</del> LY GSDKSCRMLL
151	200
HEDG4	LIGASWLISL VLGG <del>L</del> PILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
HEDG4#36	LIGASWLISL VLGG <del>L</del> PILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
REDG4	LIGASWLISL <del>VL</del> GG <del>L</del> PILGW NCL <del>D</del> HLEACS TVLPLYAKHY VLCVVTIFSI
201	250
HEDG4	ILLAVV <del>A</del> LYV RIYCVVRSSH ADMAAPQ <del>T</del> LA LLKTVTIVLG VFIVCWLP <del>A</del> F
HEDG4#36	ILLAVV <del>A</del> LYV RIYCVVRSSH ADMAAPQ <del>T</del> LA LLKTVTIVLG VFIVCWLP <del>A</del> F
REDG4	ILL <del>A</del> IVAL <del>A</del> LYV RIY <del>F</del> VVRSSH AD <del>V</del> AGP <del>T</del> LA LLKTVTIVLG VF <del>I</del> ICWLP <del>A</del> F
251	300
HEDG4	S <del>I</del> LLDYACP VHSCPILYKA HYXF <del>A</del> VSTLN SLLNPVI <del>Y</del> TW RSRDLRRE <del>V</del> L
HEDG4#36	S <del>I</del> LLDYACP VHSCPILYKA HY <del>L</del> F <del>A</del> VSTLN SLLNPVI <del>Y</del> TW RSRDLRRE <del>V</del> L
REDG4	S <del>I</del> LLD <del>S</del> TCP VR <del>A</del> CPVLYKA HY <del>E</del> F <del>A</del> F <del>A</del> TLN SLLNPVI <del>Y</del> TW RSRDLRRE <del>V</del> L
301	350
HEDG4	RPLQCWRPGV GVQGRRRG <del>G</del> GTGHLLPLRS SSSLERGMHM PTSPTFLEG <del>N</del>
HEDG4#36	RPLQCWRPGV GVQGRRRG <del>G</del> GTGHLLPLRS SSSLERGMHM PTSPTFLEG <del>N</del>
REDG4	RPLLCWRQ <del>G</del> K GATG.RRG <del>G</del> N PGHRL <del>L</del> PLRS SSSLERGLHM PTSPTFLEG <del>N</del>
351	
HEDG4	TVV-
HEDG4#36	TVV-
REDG4	TVV-

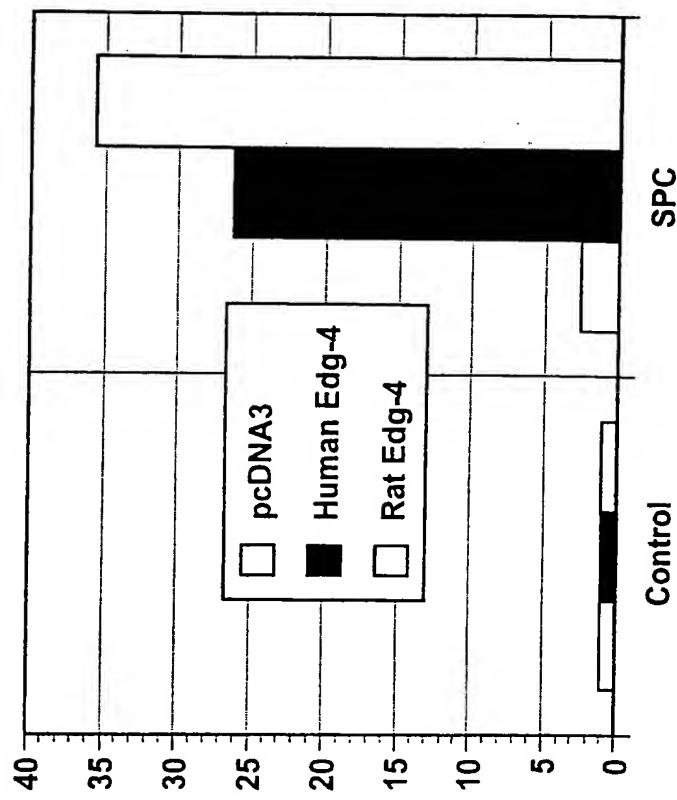


Figure 18A.

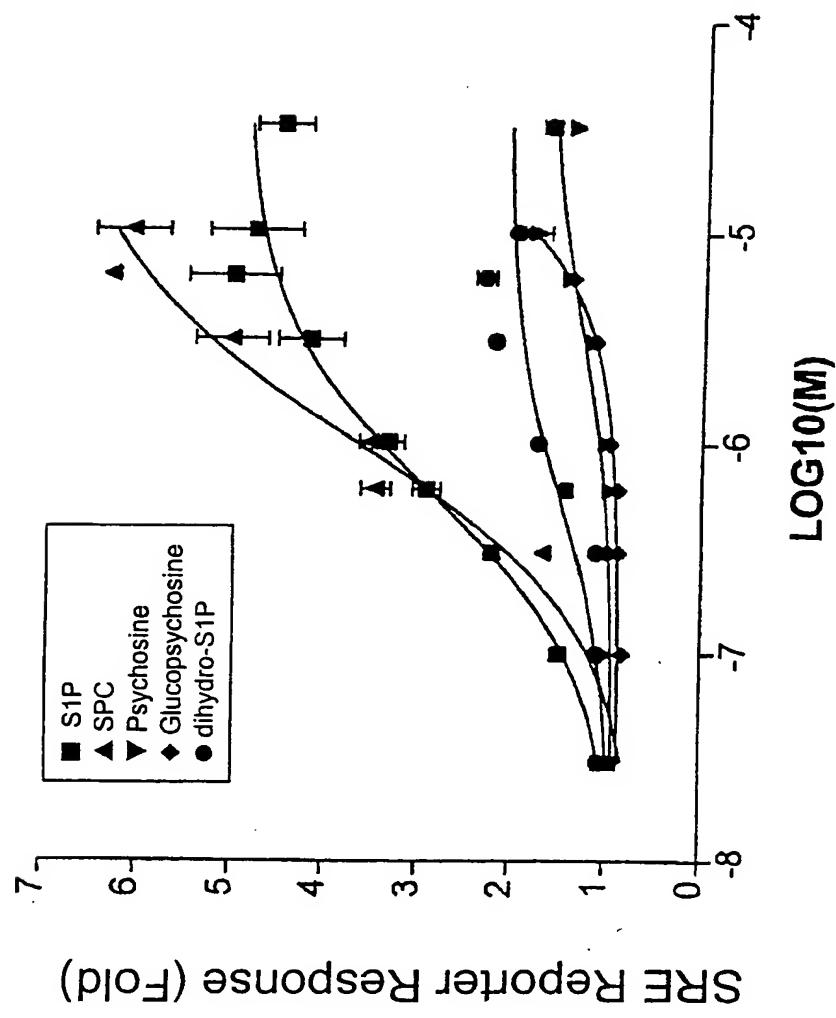


Figure 18B.

Figure 19.

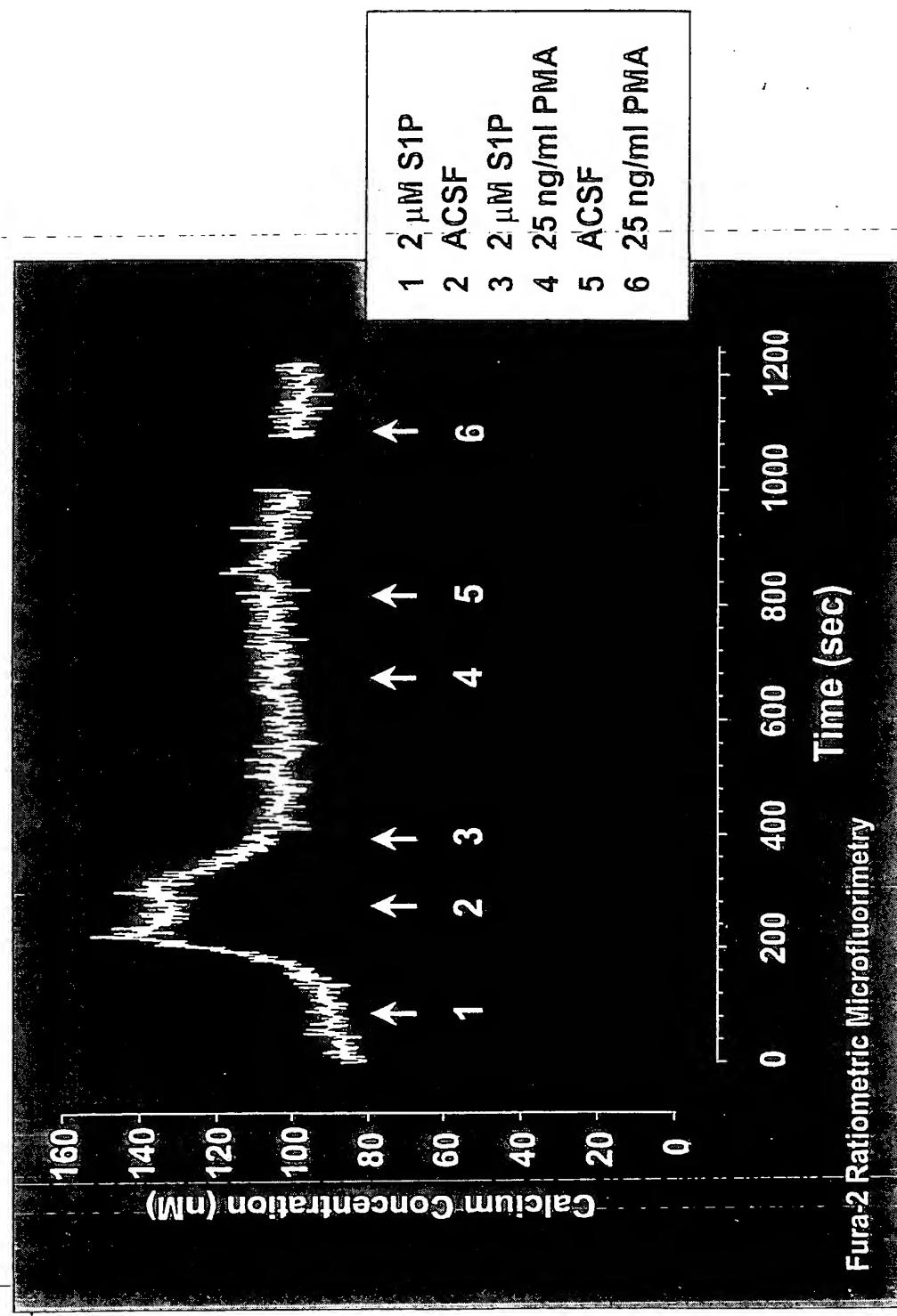


Figure 20.

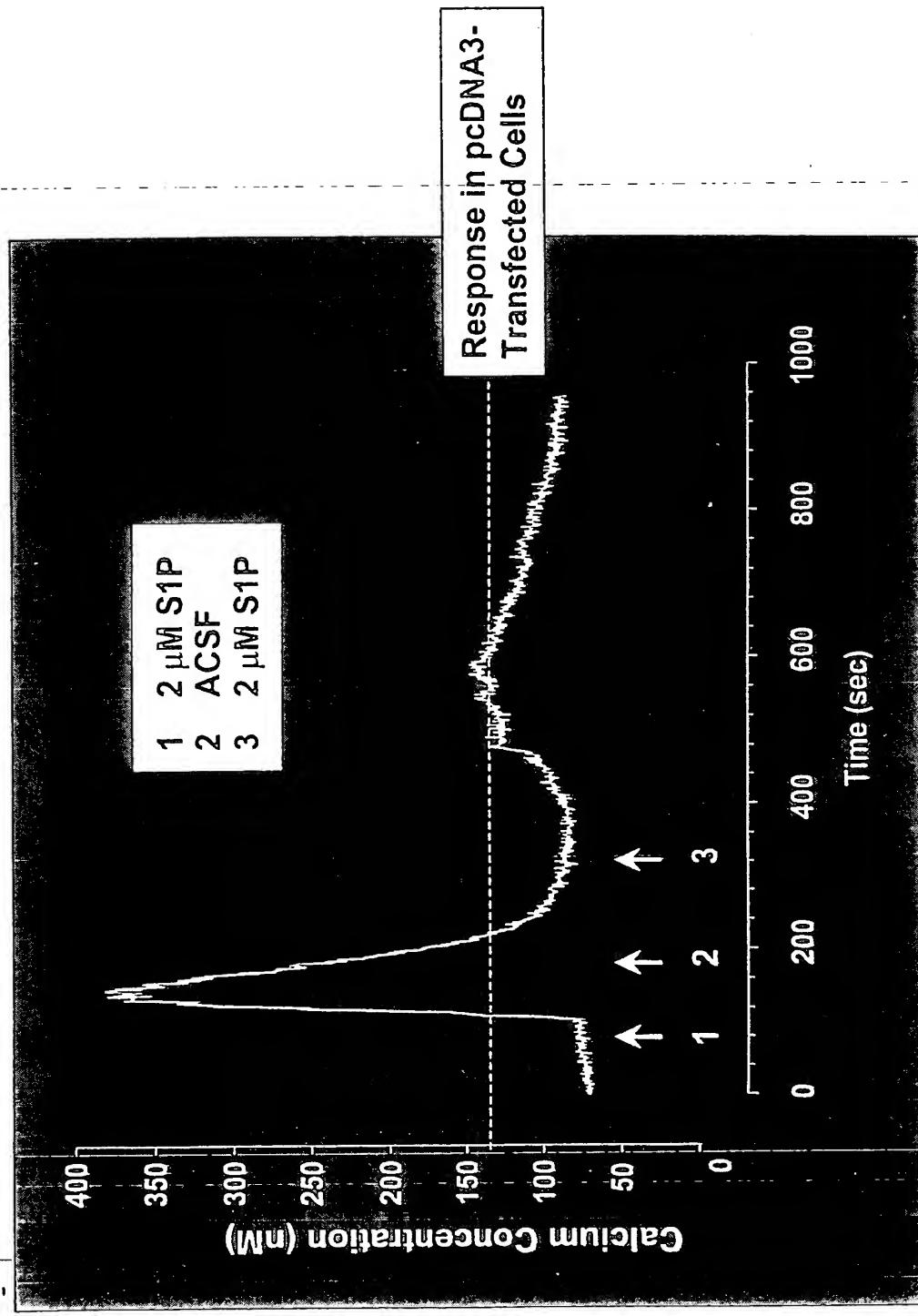


Figure 21. Human Edg-6 Amino Acid Sequence.

1	MVIMGQCYYNETIGFFYNNSGKELSSHWRPKDVVVVALGLTVSVLVLLTNLLVIAIASN	60
61	RRFHQPIYYLLGNLAAADLFAGVAYLFLMFHTGPRTRALSLEGWFLRQGLLDTSLTASVA	120
121	TLLAIAVERHRSVMAVQLHSRLPRGRVVMLIVGVWVAALGLGLLPAHSHCLCALDRCSR	180
181	MAPLLSRSYLAVALSSLLVFLLMVAVYTRIFFYVRRRVQRMAEHVSCHPRYRETTLSLV	240
241	KTVVIIILGAFVVCWTPGQVVLLLDGLGCESCNVLAVEKYFLLAEANSLVNAAVYSCRDA	300
301	EMRRTFRRLLCCACLRQSTRESVHYTSSAQGGASTRIMLPENGHPLMDSTL*	352

Figure 22. Human Edg-6 Sequence

ATGGTCATCATGGGCCAGTGC	ACTACAACGAGACCATGGCTTCTTCTATAACAA	AGT	60
1 TACCA	GTAGTACCCGGTCACGATGATGTTGCTCTGGT	AGCGAAGAAGATATTGTTGTCA	
GGCAAAGAGCTCAGCTCCACTGGCGGCCAAGGATGTGGTGTGGCACTGGGCTG	61 CCGTTTCTCGAGTCGAGGGTGACCGCCGGTTCCTACACCAGCACCACCGTGACCCGAC	120	
ACCGTCAGCGTGTGGTGTGCTGACCAATCTGCTGGT	121 TAGCAGCCATGCCCTCCAAC TGGCAGTCGCACGACCACGACACTGGTAGACGACCAGTATCGTCGGTAGCGGAGGTTG	180	
CGCCGCTTCCACCAGCCCATCTACTACCTGCTCGGCAATCTGGCCGCGCTGACCTCTTC	181 CGGGCGAAGGTGGTCGGTAGATGATGGACGAGCCGTTAGACCGGCGCCACTGGAGAAG	240	
GCGGGCGTGGCCTACCTCTTCATGTTCCACACTGGTCCCCGACAGCCCACACTTCA	241 CGCCCGCACCGGATGGAGAAGGAGTACAAGGTGTGACCAGGGCGTGTGGCTGAAAGT	300	
CTTGAGGGCTGGTTCTGCGGCAGGGCTTGCTGGACACAAGCCTCACTGCGTCGGTGGCC	301 GAACTCCCACCAAGGACGCCGTCCGAACGACCTGTGTTGGAGTGACGCCAGCCACCGG	360	
ACACTGCTGCCATGCCGTGGAGCGGCACCGCAGTGTGATGCCGTGCAGCTGCACAGC	361 TGTGACGACCGGTAGCGGCACCTCGCCGTGGCGTCAACACTACCGCACGTCACGTGTCG	420	
CGCCTCCCCGTGGCCGCGTGGTCATGCTCATTGTCGGCGTGTGGCTGCCCTGGC	421 GCGGACGGGGCACCGCGCACCAGTACGAGTAACACCCGCACACCCACCGACGGGACCCG	480	
CTGGGGCTGCTGCCCTGCCACTCCTGGCACTGCCCTGTGCCCTGGACCGCTGCTCACGC	481 GACCCGACGACGGACGGGTGAGGACCGTGACGGAGACACGGGACCTGGCGACGAGTGC	540	
ATGGCACCCCTGCTCAGCCGCTCTATTGGCCGTCTGGCTCTGTCGAGCCTGCTTGTC	541 TACCGTGGGACGAGTCGGCGAGGATAAACCGGCAGACCCGAGACAGCTCGGACGAACAG	600	
TTCCTGCTCATGGTGGCTGTGTACACCCGATTTCTTCTACGTGCGGGCGAGTGCAG	601 AAGGACGAGTACCAACCGACACATGTGGCGTAAAGAAGATGCACGCCGCGTCACGTC	660	
CGCATGGCAGAGCATGTCAGCTGCCACCCCGTACCGAGAGACCGCTCAGCCTGGTC	661 GCGTACCGTCTCGTACAGTCGACGGTGGGGCGATGGCTCTGGTGCAGTCGGACCA	720	
AAGACTGTTGTACATCATCCTGGGGCGTCTGGTGTGCTGGACACCAGGCCAGGTGGTA	721 TTCTGACAACAGTAGTAGGACCCCGCAAGCACCAGACGACCTGTGGTCCGGTCAACCAT	780	
CTGCTCCTGGATGGTTAGGCTGTGAGTCTGCAATGTCCTGGCTGTAGAAAAGTACTTC	781 GACGAGGACCTACCAAATCCGACACTCAGGACGTTACAGGACCGACATTTTCATGAAG	840	

841 CTACTGcTGGCCGAGGCCAACTCACTGGTCAATGCTGCTGTACTCTGCCGAGATGCT  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
GATGACgACCGGCTCCGGTTGAGTGACCAGTTACGACGACACATGAGAACGGCTTACGA  
901 GAGATGCCCGCACCTTCCGCCCTCTCTGCTGCGCGTGCCTCCGCCAGTCCACCCGC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
CTCTACGCCGTGGAAGGCGCGGAAGAGACGACGCCACGGAGGCGGTCAAGGTGGCG  
961 GAGTCTGTCCACTATACATCCTCTGCCAGGGAGGTGCCAGCACTCGCATCATGCTTCCC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
CTCAGACAGGTGATATGTAGGAGACGGGTCCCTCACGGTCGTGAGCGTAGTACGAAGGG  
1021 GAGAACGCCACCCACTGATGGACTCCACCCCTTAG  
-----+-----+-----+-----+-----+-----+-----+-----+  
CTCTGCCGGTGGGTGACTACCTGAGGTGGGAAATC 1056

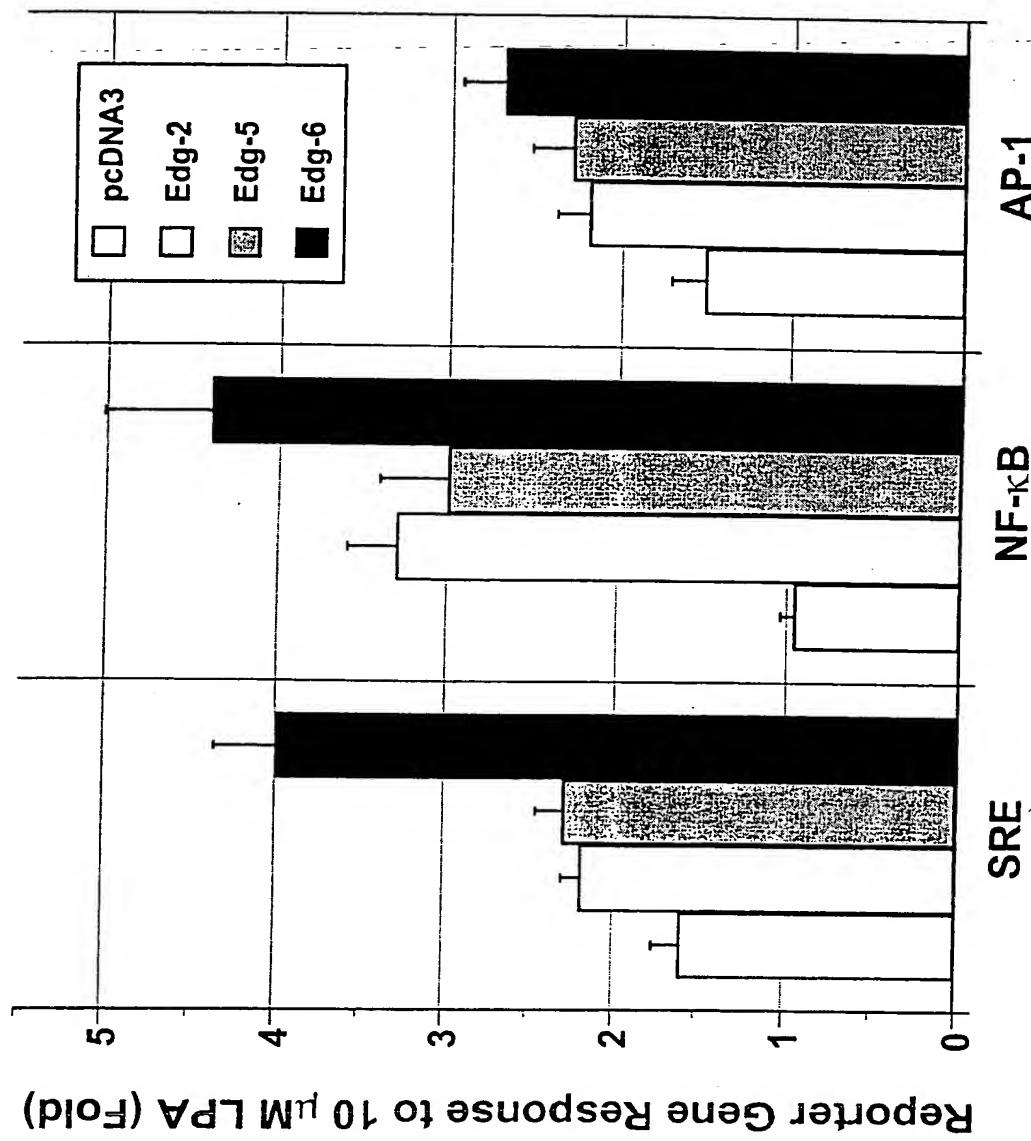


Figure 23.

Figure 24.

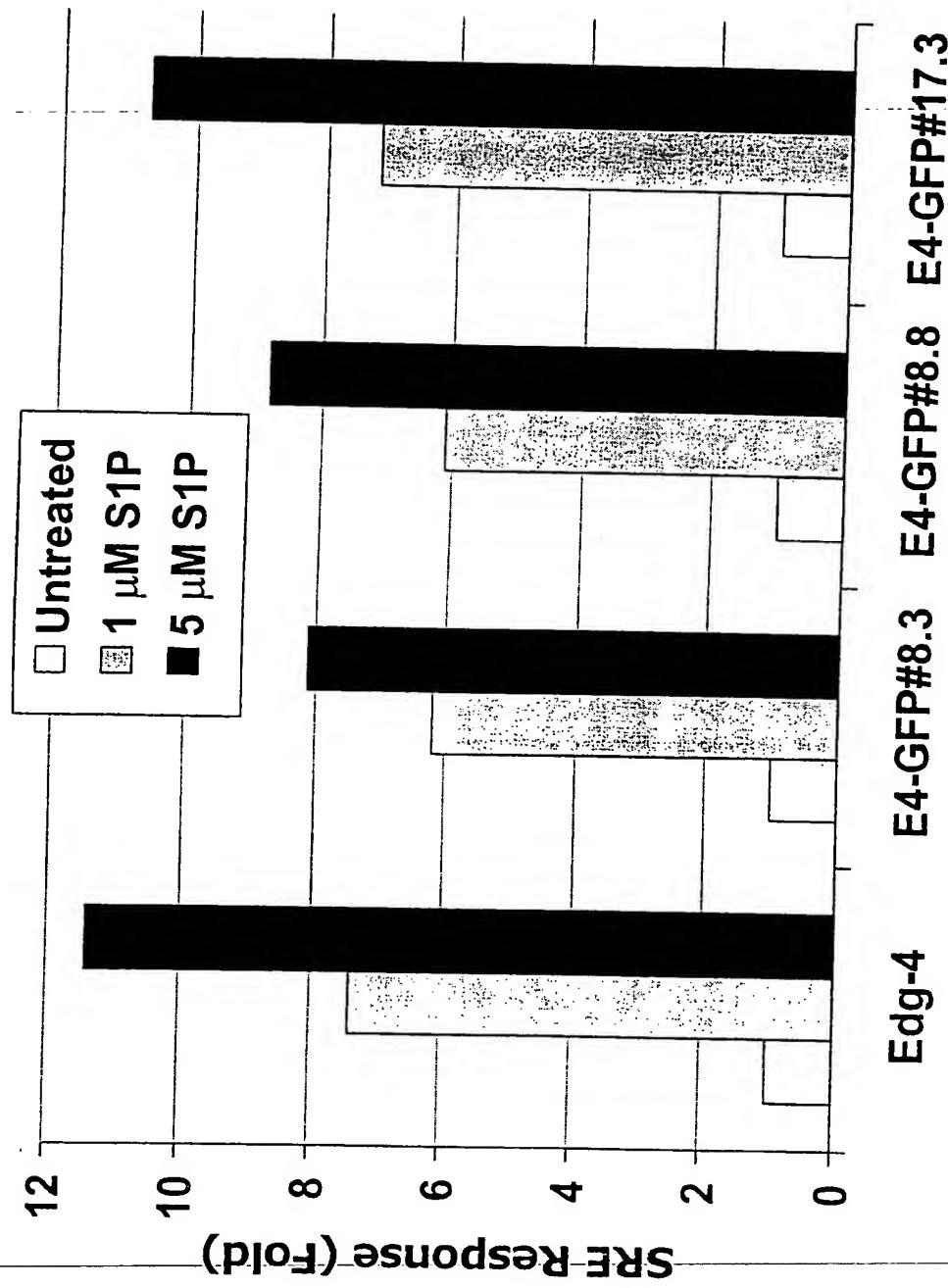


Figure 25.

